

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:40:32 : Search time 51 seconds
(without alignments)
56,562 Million cell updates/sec

Title: US-09-856-070-17

Period score: 69

Sequence: 1 EREKEQMREKEEL 14

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_orqanelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	152	4 Q9UJ22	Q9UJ22 homo sapien
2	69	100.0	156	4 Q9UJ28	Q9UJ28 homo sapien
3	69	100.0	158	4 Q9UJ27	Q9UJ27 homo sapien
4	69	100.0	159	4 Q9UJ26	Q9UJ26 homo sapien
5	69	100.0	161	4 Q9UJ20	Q9UJ20 homo sapien
6	69	100.0	166	4 Q9UJ24	Q9UJ24 homo sapien
7	66	95.7	455	11 Q9UJ43	Q9UJ43 rattus norv
8	66	95.7	585	13 Q9UJ46	Q9UJ46 gallus gall
9	66	95.7	586	11 Q9UJ41	Q9UJ41 mus musculu
10	51	73.9	556	5 Q18181	Q18181 caenorhabdi
11	51	73.9	577	11 Q35763	Q35763 rattus norv
12	51	73.9	580	13 Q9UJ71	Q9UJ71 xenopus lae
13	51	73.9	583	11 Q9UJ27	Q9UJ27 mus sp. rad
14	51	73.9	583	13 Q9UJ45	Q9UJ45 gallus gall
15	51	73.9	1326	4 Q9UJ29	Q9UJ29 homo sapien
16	47	68.1	565	5 Q9UJ28	Q9UJ28 drosophila

ALIGNMENTS

RESULT 1

Q9UJ22

ID Q9UJ22 PRELIMINARY: PRT: 152 AA.

AC Q9UJ22

DT 01-MAY-2000 (TRFMBHrel. 13, Created)

DT 01-MAY-2003 (TRFMBHrel. 13, last sequence update)

DI 01-MAR-2002 (TRFMBHrel. 20, last annotation update)

DE Cytochrome c 2 (Fragment).

GN VIL2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Chen Z.C., Radcliff A., Naftolin F.;

RI "Mutation of cytochrome c gene in glioblastoma."

RI Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF190059; AAF03158.1; .

DR InterPro: IPR000299; Band 4.1.

DR InterPro: IPR000798; Ez/rad/moesin.

DR Pfam: PF00769; FRM; 1.

DR PROSITE: PS50057; BAND_41_3; 1.

FT NON_TER 1

FT NON_TER 152

SL SEQUENCE 152 AA, 18416 MW, 875.8 kDa, 152 kDa

Query Match

Best Local Similarity 100.0%

Score 69, db 4, length 152

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMREKEEL 14

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

DB 134 EREKEQMREKEEL 147

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ID Q9UJZ8 PRELIMINARY: PRT: 156 AA.
AC Q9UJZ8:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBlrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Chen Z.C., Fadiel A., Naftolin F.;
RT "Mutation of ezrin gene in cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188896; AAF03154.1; -.
DR InterPro: IPR000299; Hand_4.1.
DR Intron: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; HAND_41_3; 1.
FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA; 19042 MW; 159F5AA684A2C3A6 CRC64;

Query Match 100.0%; Score 69; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMMREKEEL 14
DB 138 EREKEQMMREKEEL 151

RESULT 3
Q9UJZ7 PRELIMINARY: PRT: 158 AA.
ID Q9UJZ7:
AC Q9UJZ7:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBlrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RA Chen Z.C., Fadiel A., Naftolin F.;
RT "Ezrin gene mutation in ovarian cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188897; AAF03155.1; -.
DR InterPro: IPR000299; Hand_4.1.
DR Intron: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; HAND_41_3; 1.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA; 19086 MW; 86F92E1BC6F2957E CRC64;

Query Match 100.0%; Score 69; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMMREKEEL 14
DB 137 EREKEQMMREKEEL 150

RESULT 4
Q9UJZ6 PRELIMINARY: PRT: 159 AA.
ID Q9UJZ6:
AC Q9UJZ6:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBlrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Chen Z.C., Fadiel A., Naftolin F.;
RT "Mutation of ezrin gene in cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188923; AAF03156.1; -.
DR InterPro: IPR000299; Hand_4.1.
DR Intron: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; HAND_41_3; 1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 19234 MW; 7C398388B7BA70FA CRC64;

Query Match 100.0%; Score 69; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMMREKEEL 14
DB 137 EREKEQMMREKEEL 150

RESULT 5
Q9UJZ5 PRELIMINARY: PRT: 161 AA.
ID Q9UJZ5:
AC Q9UJZ5:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBlrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RA Chen Z.C., Fadiel A., Naftolin F.;
RT "Mutation analysis of ezrin gene in cancer cells.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF187552; AAU56713.1; -.
DR InterPro: IPR000299; Hand_4.1.
DR Intron: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Hand_41; 1.
DR PROSITE: PS50057; HAND_41_3; 1.
FT NON_TER 1
FT NON_TER 161
SQ SEQUENCE 161 AA; 19439 MW; 5FD6EB910E017099 CRC64;

Query Match 100.0%; Score 69; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMMREKEEL 14
DB 143 EREKEQMMREKEEL 156

RESULT 6
Q96C08 PRELIMINARY: PRT: 586 AA.
ID Q96C08:
AC Q96C08:

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DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE Similar to villin 2 (ezrin).
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SHQUNCE FROM N.A.
RC STRAUSBERG R.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC013908; AAL14904.1;
DR InterPro: IPR000299; Band_4.1;
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Band_4.1; 1.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS00660; BAND_41_1; UNKNOWN_1.
DR PROSITE: PS00661; BAND_41_2; UNKNOWN_1.
DR PROSITE: PS00557; BAND_41_3; 1.
SQ SEQUENCE 586 AA; 69412 MW; F1H592CF49A7CC46 CRC64;

Query Match 100.0%; Score 69; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMRKEEL 14
DB 334 EREKEQMRKEEL 347
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RESULT 7
Q8VHK3 PRELIMINARY; PPT; 455 AA.
AC Q8VHK3;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE Adult male kidney cDNA, P1KEN full-length enriched library,
DE Ezrin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Patton;
OX NCBI_TaxID=10116;
RN [1]
RP SHQUNCE FROM N.A.
RC STRAIN-SPPACUP-DAMIPV.
RL Submitted (Nov-2001) to the EMBL/GenBank/DBJ databases
RL EMBL: AF450298; AAL47844.1; 1.
DR InterPro: IPR000299; Band_4.1;
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Band_4.1; 1.
DR Pfam: PF00769; ERM; 1.
DR PRINTS: PR00935; BAND41.
DR SMART: SM00295; B41; 1.
DR PROSITE: PS00660; BAND_41_1; UNKNOWN_1.
DR PROSITE: PS00661; BAND_41_2; UNKNOWN_1.
DR PROSITE: PS00557; BAND_41_3; 1.
FT NON_TER 455 455
SQ SEQUENCE 455 AA; 54174 MW; 1FC9A95F4C7D5893 CRC64;

Query Match 95.7%; Score 66; DB 11; Length 455;
Best Local Similarity 92.9%; Pred. No. 0.047;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMRKEEL 14
DB 334 EREKEQMRKEEL 347
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RESULT 8
Q9YCW6 PRELIMINARY; PPT; 585 AA.
AC Q9YCW6;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DE Similar to villin 2 (ezrin).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STPAIN-WHITE LEGHORN; TISSUE-BRAIN;
RL MEDLINE 95171943; PubMed-10051754;
RA Takahashi M., Yamagata M., Noda M.;
RT "Specific expression of ezrin, a cytoskeletal membrane linker protein,
RT in a subset of chick retinorectal and sensory projections";
RL Eur. J. Neurosci. 11:545-558(1999).
DR EMBL: AB010790; BAAY5497.1; 1.
DR InterPro: IPR000299; Band_4.1;
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Band_4.1; 1.
DR Pfam: PF00769; ERM; 1.
DR PRINTS: PR00235; RAND41.
DR SMART: SM00295; B41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS00557; BAND_41_3; 1.
SQ SEQUENCE 585 AA; 69366 MW; 854C6348F783AEC CRC64;

Query Match 95.7%; Score 66; DB 13; Length 585;
Best Local Similarity 92.9%; Pred. No. 0.058;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMRKEEL 14
DB 334 EREKEQMRKEEL 347
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RESULT 9
Q9DC11 PRELIMINARY; PPT; 585 AA.
AC Q9DC11;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE Adult male kidney cDNA, P1KEN full-length enriched library,
DE close homologs7B22, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-KIDNEY.
RL MEDLINE 21085860; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kusukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Hatalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King R., Kochiwa H.,
RA Kuch S., Lewis S., Matsuo Y., Nikaido I., Pesore G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Hu J., Ketcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ping R., Pinquard M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK002756; BAB22341.1;
 DR MGI: MGI:98941; V112.
 DR InterPro: IPR000299; Band_4.1.
 DR InterPro: IPR000798; Ez/rad/moesin
 DR Pfam: PF00373; Band_4.1;
 DR Pfam: PF00769; FRM; 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; R41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00557; BAND_41_3; 1.
 SQ SEQUENCE 586 AA; 64434 MW; 561AA00457560054E CRC64;

Query Match 95.7%; Score 66; DB 11; Length 586;
 Best Local Similarity 92.0%; Pred. No. 0.058;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EREKEQMMREKEEL 14
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 Db 334 EREKEQMMREKEEL 347

RESULT 10

Q18181
 ID Q18181 PRELIMINARY; PPT: 556 AA
 AC Q18181;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE Hypothetical 61.8 kDa protein.
 GN C25H3.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Telodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 OX 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RC MF01LINE-60069611; PubMed-0851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RL 12
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Johnson D., Wilson R.;
 RT "The sequence of C. elegans cosmid C25H3.";
 RL Submitted (JUN 1995) to the EMBL/GenBank/DBJ databases.
 RN 13
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U29635; AAK31458.1;
 DR InterPro: IPR003617; TFS2_N.
 DR SMART: SM00509; TFS2N, 1.
 KW Hypothetical protein.
 SQ SEQUENCE 556 AA; 61825 MW; 7033611464040f75 CRC64;

Query Match 73.9%; Score 51; DB 5; Length 556;
 Best Local Similarity 83.3%; Pred. No. 8.7;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EREKEQMMREKEEL 12
 |||||:|||||
 Db 409 EREKEQMMREKEEL 420

RESULT 11

G35763
 ID G35763 PRELIMINARY; PPT: 577 AA.
 AC G35763;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Moesin.
 OS Mus musculus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 OX 11
 RP SEQUENCE FROM N.A.
 RC MF01LINE-20404063; PubMed-10945828;
 RA Theodorides T.C., Wang L., Pang X., Letourneau R., Culm K.E., Basu S.,
 RA Wang Y., Correia I.;
 RT "Cloning and cellular localization of the rat mast cell 78 kDa protein
 RT phosphorylated in response to the mast cell stabilizer cromolyn.";
 RL J. Pharmacol. Exp. Ther. 294: 810-820(2000)
 DR EMBL: AF004811; AA061666.1;
 DR InterPro: IPR000299; Band_4.1.
 DR InterPro: IPR000798; Ez/rad/moesin.
 DR Pfam: PF00373; Band_41; 1.
 DR Pfam: PF00769; FRM; 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; R41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00557; BAND_41_3; 1.
 SQ SEQUENCE 577 AA; 67739 MW; 49F4797406C8F6C8 CRC64;

Query Match 73.9%; Score 51; DB 11; Length 577;
 Best Local Similarity 71.4%; Pred. No. 9;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OY 1 EREKEQMMREKEEL 14
 |||||:|||||
 Db 334 EREKEQMMREKEEL 347

RESULT 12

G9PT71
 ID G9PT71 PRELIMINARY; PPT: 580 AA.
 AC G9PT71;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2002 (TrEMBLrel. 20, last annotation update)
 DE Moesin.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 OX 11
 RP SEQUENCE FROM N.A.
 RC Armstrong N.A., Thern J.M., Kay B.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U25763; AAF31215.1;
 DR InterPro: IPR000299; Band_4.1.
 DR InterPro: IPR000798; Ez/rad/moesin.
 DR Pfam: PF00373; Band_41; 1.
 DR Pfam: PF00769; FRM; 1.
 DR PRINTS: PR00935; BAND41.
 DR SMART: SM00295; R41; 1.
 DR PROSITE: PS00661; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00557; BAND_41_3; 1.
 SQ SEQUENCE 580 AA; 68134 MW; 1006A7E9E5887074 CRC64;

Query Match 73.9%; Score 51; DB 13; Length 580;
 Best Local Similarity 71.4%; Pred. No. 9;

